

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.  
Bandman, Olga
- (ii) TITLE OF THE INVENTION: NOVEL RAB PROTEINS
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0183 US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-845-4166  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: Consensus  
(B) CLONE: Consensus

09988974-11904

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Asp Ser Glu Glu Glu Ser Gln Asp Arg Gln Leu Lys Ile Val  
 1 5 10 15  
 Val Leu Gly Asp Xaa Ala Ser Gly Lys Thr Ser Leu Thr Thr Cys Phe  
 20 25 30  
 Ala Gln Glu Thr Phe Gly Lys Gln Tyr Lys Gln Thr Ile Gly Leu Asp  
 35 40 45  
 Phe Phe Leu Arg Arg Ile Thr Leu Pro Gly Asn Leu Asn Val Thr Leu  
 50 55 60  
 Gln Ile Trp Asp Ile Gly Gly Gln Thr Ile Gly Gly Lys Met Leu Asp  
 65 70 75 80  
 Lys Tyr Ile Tyr Gly Ala Gln Gly Val Leu Val Tyr Asp Ile Thr  
 85 90 95  
 Asn Tyr Gln Ser Phe Glu Asn Leu Glu Asp Trp Tyr Thr Val Val Lys  
 100 105 110  
 Lys Val Ser Xaa Glu Ser Glu Thr Gln Pro Leu Val Ala Leu Val Gly  
 115 120 125  
 Asn Lys Ile Asp Leu Glu His Met Arg Thr Ile Lys Pro Glu Lys His  
 130 135 140  
 Leu Arg Phe Cys Gln Glu Asn Gly Phe Ser Ser His Phe Val Ser Ala  
 145 150 155 160  
 Lys Thr Gly Asp Ser Val Phe Leu Cys Phe Gln Lys Val Ala Ala Glu  
 165 170 175  
 Ile Leu Gly Ile Lys Leu Asn Xaa Xaa Gln Xaa Xaa Xaa Ser His Xaa  
 180 185 190  
 Gly Val Val Lys Xaa Xaa Ile Val Asn Tyr Asn Gln Glu Pro Met Ser  
 195 200 205  
 Arg Thr Xaa Asn Pro Pro Arg Ser Ser Met Cys Ala Val Gln  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGCTTG CCGAGTGATT CTCCTCGAAT ACCTCCTGCC GGCGCGGAGA CACCGGGGCG 60  
 GGGGTCCTGC CGCAACTACC TCCCTTCCTC CTCTCCCCCG CCCCCGGAGC CTTTCATCCTT 120  
 CCCTTCCCCC CCCACCTCGA GGGGCGGGCC TGGTTCCCGG GACACCATGT CGGACTCTGA 180  
 GGAGGAGAGC CAGGACCGGC AACTGAAAAT CGTCGTGCTG GGGGACGNNG CCTCCGGGAA 240  
 GACCTCCTTA ACTACGTGTT TTGCTCAAGA AACTTTTGGG AAACAGTACA AACAAACTAT 300  
 AGGACTGGAT TTCTTTTGA GAAGGATAAC ATTGCCAGGA AACTTGAATG TTACCCCTTCA 360  
 AATTTGGGAT ATAGGAGGGC AGACAATAGG AGGCAAAATG TTGGATAAAT ATATCTATGG 420  
 AGCACAGGGA GTCCTCTTGG TATATGATAT TACAAATTAT CAAAGCTTTG AGAATTTAGA 480  
 AGATTGGTAT ACTGTGGTGA AGAAAGTGAG CNAGGAGTCA GAAACTCAGC CACTGGTTGC 540  
 CTTGGTAGGC AATAAAATTG ATTTGGAGCA TATGCGAACA ATAAACCTG AAAAACACTT 600  
 ACGGTTTTGC CAGGAAAATG GTTTTAGTAG CCACCTTGTC TCAGCCAAGA CAGGAGACTC 660  
 TGTCTTCCTG TGCTTTCAGA AAGTTGCTGC TGAAATCCTT GGGATCAAAT TAAACAANNA 720  
 GCAGAAWTRG MACAGTCACA GWGGGGTGGT GAAGGSAGRT ATTGTAAACT ACAACCAGGA 780  
 ACCTATGTCA AGGACTKTTA ACCCTCCTAG AAGCTCTATG TGTGCAGTTC AGTGAGCGCA 840  
 TTTTNCCTTT GTNTTGATAG TTCTGGCTGC CCTTCAACTC TGGGTGGGNC CCNAGGGCTT 900  
 CTAGGACTTG TTTT 914

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Xaa Lys Met Gly Asn Gly Thr Glu Glu Asp Tyr Asn Phe Val  
 1 5 10 15  
 Phe Lys Val Val Leu Ile Gly Glu Ser Gly Val Gly Lys Thr Asn Leu  
 20 25 30  
 Leu Ser Arg Phe Thr Arg Asn Glu Phe Ser His Asp Ser Arg Thr Thr  
 35 40 45  
 Ile Gly Val Glu Phe Ser Thr Arg Thr Val Met Leu Gly Thr Ala Ala  
 50 55 60  
 Val Lys Ala Gln Ile Trp Asp Thr Ala Gly Leu Glu Arg Tyr Arg Ala  
 65 70 75 80  
 Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val Phe  
 85 90 95  
 Asp Leu Thr Lys His Gln Thr Tyr Ala Val Val Glu Arg Trp Leu Lys  
 100 105 110  
 Glu Leu Tyr Asp His Ala Glu Ala Thr Ile Val Val Met Leu Val Gly  
 115 120 125  
 Asn Lys Ser Asp Leu Ser Gln Gly Arg Glu Val Pro Thr Glu Glu Ala  
 130 135 140  
 Arg Met Phe Ala Glu Asn Asn Gly Leu Leu Phe Leu Glu Thr Ser Ala  
 145 150 155 160  
 Leu Asp Ser Thr Asn Val Glu Leu Ala Phe Glu Thr Val Leu Lys Glu  
 165 170 175  
 Ile Phe Ala Lys Val Ser Lys Gln Arg Gln Asn Ser Ile Arg Thr Asn  
 180 185 190  
 Ala Ile Thr Leu Gly Ser Ala Gln Xaa Gly Gln Glu Pro Gly Pro Gly  
 195 200 205  
 Glu Lys Arg Ala Cys Cys Ile Ser Leu  
 210 215

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCATTGAGC CAACACACAG ATTTGTGCGC TCTGTCCCCG AAGACACCTG CACCCTCCAT 60  
 GCGGANCAAG ATGGGGAATG GAACTGAGGA AGATTATAAC TTTGTCTTCA AGGTGGTGCT 120  
 GATCGGCGAA TCAGGTGTGG GGAAGACCAA TCTACTCTCC CGATTACGC GCAATGAGTT 180  
 CAGCCACGAC AGCCGCACCA CCATCGGGGT TGAGTTCTCC ACCCGCACTG TGATGTTGGG 240

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 201 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) LIBRARY: Consensus  
(B) CLONE: Consensus

Met	Ala	Gly	Lys	Ser	Ser	Leu	Phe	Lys	Val	Ile	Leu	Leu	Gly	Asp	Gly
1				5					10					15	
Gly	Val	Gly	Lys	Ser	Ser	Leu	Met	Asn	Arg	Tyr	Val	Thr	Asn	Lys	Phe
			20					25					30		
Asp	Thr	Gln	Leu	Phe	His	Thr	Ile	Gly	Val	Glu	Phe	Leu	Asn	Lys	Asp
		35					40					45			
Leu	Glu	Val	Asp	Gly	His	Phe	Val	Thr	Met	Gln	Ile	Trp	Asp	Thr	Ala
	50					55					60				
Gly	Gln	Glu	Arg	Phe	Arg	Ser	Leu	Arg	Thr	Pro	Phe	Tyr	Arg	Gly	Ser
65					70					75				80	
Asp	Cys	Cys	Leu	Leu	Thr	Phe	Ser	Val	Asp	Asp	Ser	Gln	Ser	Phe	Gln
				85					90					95	
Asn	Leu	Ser	Asn	Trp	Lys	Lys	Glu	Phe	Ile	Tyr	Tyr	Ala	Asp	Val	Lys
			100					105					110		
Glu	Pro	Glu	Ser	Phe	Pro	Phe	Val	Ile	Leu	Gly	Asn	Lys	Ile	Asp	Ile
			115				120					125			
Ser	Glu	Arg	Gln	Val	Ser	Thr	Glu	Glu	Ala	Gln	Ala	Trp	Cys	Arg	Asp
	130					135					140				
Asn	Gly	Asp	Tyr	Pro	Tyr	Phe	Glu	Thr	Ser	Ala	Lys	Asp	Ala	Thr	Asn
145					150					155					160
Val	Ala	Ala	Ala	Phe	Glu	Glu	Ala	Val	Arg	Arg	Val	Leu	Ala	Thr	Glu
				165					170					175	
Asp	Arg	Ser	Asp	His	Leu	Ile	Gln	Thr	Asp	Thr	Val	Asn	Leu	His	Arg
			180					185					190		
Lys	Pro	Lys	Pro	Ser	Ser	Ser	Cys	Cys							
		195					200								

(A) LENGTH: 1175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus  
(B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACTGTGATG AAACACTTTT CCCGTGTCGT TTGAGTGCAT CTTCTCAACA ACCCTAGGAG 60  
GGTTCCTTGAA GCTTTTGAAGA TTAACAATGG CAGGAAAATC ATCACTTTTT AAAGTAATTC 120  
TCCTTGAGAGA TGGTGGAGTT GGAAGAGTT CACTTATGAA CAGATATGTA ACTAATAAGT 180  
TTGATACCCA GCTCTTCCAT ACAATAGGTG TGGAATTTTT AAATAAAGAT TTGGAAGTGG 240  
ATGGACATTT TGTTACCATG CAGATTTGGG ACACGGCAGG TCAGGAGCGA TTCCGAAGCC 300  
TGAGGACACC ATTTTACAGA GGTCTGACT GCTGCCTGCT TACTTTTAGT GTCGATGATT 360  
CACAAAGCTT CCAGAACTTA AGTAACTGGA AGAAAGAATT CATATATTAT GCAGATGTGA 420  
AAGAGCCTGA GAGCTTTCCT TTTGTGATTC TGGGTAACAA GATTGACATA AGCGAACGGC 480  
AGGTGTCTAC AGAAGAAGCC CAAGCTTGGT GCAGGGACAA CGGCGACTAT CCTTATTTTG 540  
AAACAAGTGC AAAAGATGCC ACAAATGTGG CAGCAGCCTT TGAGGAAGCG GTTCCAAGAG 600  
TTCTTGCTAC CGAGGATAGG TCAGATCATT TGATTCAGAC AGACACAGTC AATCTTCACC 660  
GAAAGCCCAA GCCTAGCTCA TCTTGCTGTT GATTGTGTTAGA TTGTGATGC ATTCTAACCA 720  
ACTCACACAT ATACACAAA TCAACATGGG GATGGAGAAG AGAATTAGCG TTTGCAGCAG 780  
TGTATCATCT ACTAATAAAA TTAAACTAAT GTTGCTGCTT CATTAGTTGG TGGGAGAAGG 840  
GACACATCCA CTCTGGAGG AATATATTTA CTCAATAATG GCACCTTACA TTTATAAAAT 900  
GTAACAGTTG TCTAATAACG TTTCTTTAAT TTAAATATGT AAGTTGCAGA GCTAATAAAT 960  
GAAATGACCA AGACTTTAAT TATAATAAAA ATAAGAACT TGACTATTCT AGAAGTTATA 1020  
CTTGGATTTT TTCCTGGGAA AATGGAGAAC TACTTTTTAT ATGTGTATGT TTTTATGCAA 1080  
TTAGCATGTG ATTCTTGTT CAGGGAAATA CTTTCCTAAA GCAATAATGT TAGATATTAA 1140  
AGATTAAAAA CTAATGTAAA AAAAAAAAAA AAAAA 1175

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 1154901

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Asp Ser Glu Glu Ser Gln Asp Arg Gln Leu Lys Ile Val  
1 5 10 15  
Val Leu Gly Asp Gly Thr Ser Gly Lys Thr Ser Leu Ala Thr Cys Phe  
20 25 30  
Ala Gln Glu Thr Phe Gly Lys Gln Tyr Lys Gln Thr Ile Gly Leu Asp  
35 40 45  
Phe Phe Leu Arg Arg Ile Thr Leu Pro Gly Asn Leu Asn Val Thr Leu  
50 55 60  
Gln Val Trp Asp Ile Gly Gly Gln Thr Ile Gly Lys Met Leu Asp  
65 70 75 80  
Lys Tyr Ile Tyr Gly Ala Gln Gly Ile Leu Leu Val Tyr Asp Ile Thr  
85 90 95  
Asn Tyr Gln Ser Phe Glu Asn Leu Glu Asp Trp Tyr Ser Val Val Lys  
100 105 110  
Thr Val Ser Glu Glu Ser Glu Thr Gln Pro Leu Val Ala Leu Val Gly  
115 120 125  
Asn Lys Ile Asp Leu Glu His Met Arg Thr Val Lys Pro Asp Lys His  
130 135 140  
Leu Arg Phe Cys Gln Glu Asn Gly Phe Ser Ser His Phe Val Ser Ala  
145 150 155 160

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Lys	Thr	Gly	Asp	Ser	Val	Phe	Leu	Cys	Phe	Gln	Lys	Val	Ala	Ala	Glu
				165					170					175	
Ile	Leu	Gly	Ile	Lys	Leu	Asn	Lys	Ala	Glu	Ile	Glu	Gln	Ser	Gln	Arg
			180					185					190		
Val	Val	Lys	Ala	Asp	Ile	Val	Asn	Tyr	Asn	Gln	Glu	Pro	Met	Ser	Arg
		195					200					205			
Thr	Val	Asn	Pro	Pro	Arg	Ser	Ser	Met	Cys	Ala	Val	Gln			
210					215						220				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 436001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Asn	Gly	Lys	Glu	Glu	Asp	Tyr	Asn	Phe	Val	Phe	Lys	Val	Val
1				5					10					15	
Leu	Ile	Gly	Glu	Ser	Gly	Val	Gly	Lys	Thr	Asn	Leu	Leu	Ser	Arg	Phe
			20					25					30		
Thr	Arg	Asn	Glu	Phe	Ser	His	Asp	Ser	Arg	Thr	Thr	Ile	Gly	Val	Glu
		35					40					45			
Phe	Ser	Thr	Arg	Thr	Val	Leu	Gly	Thr	Ala	Ala	Val	Lys	Ala	Gln	
	50				55				60						
Ile	Trp	Asp	Thr	Ala	Gly	Leu	Glu	Arg	Tyr	Arg	Ala	Ile	Thr	Ser	Ala
65				70					75					80	
Tyr	Tyr	Arg	Gly	Ala	Val	Gly	Ala	Leu	Leu	Val	Phe	Asp	Leu	Thr	Lys
			85					90					95		
His	Gln	Thr	Tyr	Ala	Val	Val	Glu	Arg	Trp	Leu	Lys	Glu	Leu	Tyr	Asp
		100					105					110			
His	Ala	Glu	Ala	Thr	Ile	Val	Val	Met	Leu	Val	Gly	Asn	Lys	Ser	Asp
	115					120					125				
Leu	Ser	Gln	Ala	Arg	Glu	Val	Pro	Thr	Glu	Glu	Ala	Arg	Met	Phe	Ala
	130				135					140					
Glu	Asn	Asn	Gly	Leu	Leu	Phe	Leu	Glu	Thr	Ser	Ala	Leu	Asp	Ser	Thr
145				150					155					160	
Asn	Val	Glu	Leu	Ala	Phe	Glu	Thr	Val	Leu	Lys	Glu	Ile	Phe	Ala	Lys
		165						170					175		
Val	Ser	Lys	Gln	Ile	Gln	Asn	Ser	Pro	Arg	Ser	Asn	Ala	Ile	Ala	Leu
		180					185					190			
Gly	Ser	Ala	Gln	Ala	Gly	Gln	Glu	Pro	Gly	Pro	Gly	Gln	Lys	Arg	Ala
	195					200						205			
Cys	Cys	Ile	Asn	Leu											
210															

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

09988974-111901

PF-0183-2 DIV

(A) LIBRARY: GenBank

(B) CLONE: 486830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Gly	Lys	Ser	Ser	Leu	Phe	Lys	Val	Ile	Leu	Leu	Gly	Asp	Gly
1				5					10					15	
Gly	Val	Gly	Lys	Ser	Ser	Leu	Met	Asn	Arg	Tyr	Val	Thr	Asn	Lys	Phe
			20					25					30		
Asp	Thr	Gln	Leu	Phe	His	Thr	Ile	Gly	Val	Glu	Phe	Leu	Asn	Lys	Asp
		35				40					45				
Leu	Glu	Val	Asp	Gly	His	Phe	Val	Thr	Met	Gln	Ile	Trp	Asp	Thr	Ala
	50				55						60				
Gly	Gln	Glu	Arg	Phe	Arg	Ser	Leu	Arg	Thr	Pro	Phe	Tyr	Arg	Gly	Ser
65				70						75					80
Asp	Cys	Cys	Leu	Leu	Thr	Phe	Ser	Val	Asp	Asp	Ser	Gln	Ser	Phe	Gln
			85					90					95		
Asn	Leu	Ser	Asn	Trp	Lys	Lys	Glu	Phe	Ile	Tyr	Tyr	Ala	Asp	Val	Lys
			100					105					110		
Glu	Pro	Glu	Ser	Phe	Pro	Phe	Val	Ile	Leu	Gly	Asn	Lys	Ile	Asp	Ile
		115					120					125			
Ser	Glu	Arg	Gln	Val	Ser	Thr	Glu	Glu	Ala	Gln	Ala	Trp	Cys	Arg	Asp
	130					135					140				
Asn	Gly	Asp	Tyr	Pro	Tyr	Phe	Glu	Thr	Ser	Ala	Lys	Asp	Ala	Thr	Asn
145					150					155					160
Val	Ala	Ala	Ala	Phe	Glu	Glu	Ala	Val	Arg	Arg	Val	Leu	Ala	Thr	Glu
			165					170						175	
Asp	Arg	Ser	Asp	His	Leu	Ile	Gln	Thr	Asp	Thr	Val	Ser	Leu	His	Arg
			180					185					190		
Lys	Pro	Lys	Pro	Ser	Ser	Ser	Cys	Cys							
		195					200								

09988974-11901